

78-0B10 amino acid sequence (SEQ ID NO:1)

	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu	
5	1				5					10					15		
	Ala	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr	
				20					25					30			
	Ala	Asp	Ile	Ser	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu	
			35					40					45				
10	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu	
	50						55					60					
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys	
	65					70					75					80	
	Ser	Glu	Asn	Gly	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr	
15					85					90					95		
	Leu	Gly	Ile	Ile	Ala	Ala	Pro	Val	Ser	Asp	Lys	Tyr	Ile	Glu	Arg	Glu	
				100					105					110			
	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Ile	Phe	Cys	Ser	
			115					120					125				
20	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser	
	130						135					140					
	Val	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr	
	145					150					155					160	
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp	
25					165					170					175		
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala	
				180					185					190			
	Leu	Val	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Val	Pro	Lys	Gly	Val	Met	
		195						200					205				
30	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Leu	Ala	Lys	Asp	Pro	
	210					215						220					
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Thr	Ala	Ile	Leu	Thr	Val	Ile	
	225					230					235					240	
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr	
35					245					250					255		
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe	
			260						265					270			
	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro	
		275						280					285				
40	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp	
	290					295						300					
	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys	
	305					310					315						

	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
			435					440					445			
5	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
		450					455					460				
	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro
	465					470					475					480
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile
10				485						490					495	
	Val	Gln	Asp	Phe	Val	Ser	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
			500						505					510		
	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
		515						520					525			
15	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Phe	Glu	Lys	His	Thr	Asn	Gly
		530					535						540			

90-185 amino acid sequence (SEQ ID NO:2)

20	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
				20					25					30		
25	Ala	Asp	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35					40					45			
	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
		50					55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
30	65					70					75				80	
	Ser	Glu	Asn	Gly	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
				85						90					95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
			100						105					110		
35	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115					120					125			
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
40	145					150					155					160
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165						170					175	
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
				180					185					190		
45	Leu	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met
		195						200					205			
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Leu	Ala	Lys	Asp	Pro
		210					215						220			
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Thr	Ala	Ile	Leu	Thr	Val	Ile
50	225					230					235					240
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
				245						250					255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
				260					265					270		
55	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
		275						280						285		
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
		290					295						300			

Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys  
 305 310 315 320  
 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg  
 325 330 335  
 5 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro  
 340 345 350  
 Lys Gly Asp Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His  
 355 360 365  
 10 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn  
 370 375 380  
 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr  
 385 390 395 400  
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp  
 405 410 415  
 15 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr  
 420 425 430  
 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val  
 435 440 445  
 20 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val  
 450 455 460  
 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro  
 465 470 475 480  
 Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile  
 485 490 495  
 25 Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg  
 500 505 510  
 Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys  
 515 520 525  
 30 Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly  
 530 535 540

133-1B2 amino acid sequence (SEQ ID NO:3)

35 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu  
 1 5 10 15  
 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr  
 20 25 30  
 40 Ala Asp Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu  
 35 40 45  
 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu  
 50 55 60  
 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys  
 65 70 75 80  
 45 Ser Glu Asn Ser Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr  
 85 90 95  
 Leu Gly Ile Ile Val Ala Pro Val Asn Asp Lys Tyr Ile Glu Arg Glu  
 100 105 110  
 50 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Val Phe Cys Ser  
 115 120 125  
 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser  
 130 135 140  
 Ile Glu Thr Ile Ile Ile Leu Asp Leu Asn Asp Asp Leu Gly Gly Tyr  
 145 150 155 160  
 55 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp  
 165 170 175  
 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala  
 180 185 190

Leu Ile Met Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met  
 195 200 205  
 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Ile Ala Lys Asp Pro  
 210 215 220  
 5 Thr Phe Gly Asn Ala Ile Asn Pro Thr Ser Ala Ile Leu Thr Val Ile  
 225 230 235 240  
 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr  
 245 250 255  
 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe  
 260 265 270  
 10 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Val Pro  
 275 280 285  
 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp  
 290 295 300  
 15 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys  
 305 310 315 320  
 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg  
 325 330 335  
 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro  
 340 345 350  
 20 Lys Gly Asp Ala Lys Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His  
 355 360 365  
 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn  
 370 375 380  
 25 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Pro Met Ile Met Lys Gly Tyr  
 385 390 395 400  
 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Asp Asn Asp Gly Trp  
 405 410 415  
 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr  
 420 425 430  
 30 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val  
 435 440 445  
 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val  
 450 455 460  
 35 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro  
 465 470 475 480  
 Ala Ala Gly Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile  
 485 490 495  
 Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg  
 500 505 510  
 40 Gly Gly Val Ile Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys  
 515 520 525  
 Ile Asp Arg Lys Val Leu Arg Gln Met Leu Glu Lys His Thr Asn Gly  
 530 535 540  
 45

146-1H2 amino acid sequence (SEQ ID NO:4)

Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu  
 1 5 10 15  
 Glu Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr  
 20 25 30  
 Ala Ala Ile Pro Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu  
 35 40 45  
 55 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu  
 50 55 60  
 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys  
 65 70 75 80

	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
					85					90					95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
					100				105					110		
5	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115					120					125			
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
10	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
	145					150				155					160	
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165					170					175		
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
				180					185					190		
15	Ser	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met
			195					200					205			
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Ile	Ala	Lys	Asp	Pro
		210					215					220				
20	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Ser	Ala	Ile	Leu	Thr	Val	Ile
	225					230					235				240	
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
				245						250					255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
				260					265					270		
25	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
			275					280					285			
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
		290					295					300				
30	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
	305					310					315				320	
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
				325						330					335	
	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
				340					345					350		
35	Lys	Gly	Asp	Ala	Lys	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Leu	His
		355						360					365			
	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
		370					375					380				
40	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Pro	Met	Ile	Met	Lys	Gly	Tyr
	385					390				395					400	
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
				405						410					415	
	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
45	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
		435						440					445			
	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
		450					455					460				
50	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro
	465					470					475				480	
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile
				485						490					495	
	Val	Gln	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
			500					505						510		
55	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
			515					520					525			
	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Leu	Glu	Lys	His	Thr	Asn	Gly
		530					535						540			

73-0B10 (SEQ ID NO:5)

5 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGGTG  
ATGGGACGGGTGGAGAACAGATSTTTGACGCATTATCTCGTTATGCAGATATTTCCCGA  
TGCATAGCATTGACAAATGCTCATAACAAAAGAAAATGTTTTATATGAAGAGTTTTTAAA  
ATTGTCTGTCTGTTTAGCGGAAAGTTTTAAAAAGTATGSAATTAACAAAACGACACAA  
TAGCGGTGTGTAGCGAAAATGGTTTGCAATTTTTCTTCTGTAAATGCATCATTGTAT  
CTTGGAAATAATTGCAGCACCTGTTAGTGATAAATACATTGAACGTGAATTAATACACAG  
TCTTGGTATTGTAAAACACGCATAATTTTTTGTCCAAGAATACTTTTCAAAAAGTAC  
10 TGAATGTAAAATCTAAATTAATAATCTGTAGAAAATATTATTATATTAGACTTAAATGAA  
GACTTAGGAGSTTATCAATGGCTCAACAACCTTTATTTCTCAAAATTCGGATAGTAATCT  
GGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGCTAA  
TGTTTTCTTCTGGTACAACCTGGTGTTCGGAAGGGAGTCATGCTAACTCACAAGAAATTT  
GTTGCACGATTTTCTCTTGCAAAAGATCTTACTTTTGGTAACGCAATTAATCCACGAC  
15 AGCAATTTTAACGSTAATACCTTTCCACCATGGTTTTGGTATGATGACCACATTAGGAT  
ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAAACTATTCTTA  
CAATCATTACAAGATTATAAAGTGGAAAGTACTTTACTTGTACCAACATTAATGGCAT  
TCTTGCAAAAAGTGCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTCAT  
CTGGTGGCGCACCTTTTATCAAAAGAAATTTGGGGAGATGGTGAAAAAACGGTTTTAAATTA  
20 AACTTTGTGAGGCAAGGGTATGGATTAACAGAAACCACTTCCGCTGTTTTAATTACACC  
GAAAGGTGACGCCAGACCGGGATCAACTGGTAAAATAGTACCATTTACGCTGTAAAG  
TTGTGATCCTACAACAGGAAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTT  
AAAGGCGCCATGATAATGAAGGGTTATTATAAATGAAGAAGCTACTAAAGCAATTAAT  
TGATAATGACGGATGGTTGCGCTCTGGTGATATTGCTTATTATGACAATGATGGCCATT  
25 TTTATATTGTGGACAGGCTGAAGTCATTAATTAATATAAAGGTTATCAGGTTGCACCT  
GCTGAAATTGAGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGG  
TATACCGGATGAAGCGCGGGGAGCTTCCAGCTGCAGGTGTTCTAGTACAGACTGGAA  
AATATCTAAACGAACAAATCGTACAAGATTTTGTTCAGTCAAGTTTCAACAGCAAAA  
TGGCTACGTGGTGGGGTGAAATTTTTGGATGAAATTCCTCAAAGGATCAACTGGAAAAAT  
30 TGACAGAAAAGTGTTAAGACAAATGTTTGAAAAACACACCAATGGG

98-1B5 (SEQ ID NO:6)

35 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGGAGA  
TGGGACGGGTGGAGAACAGATSTTTGACGCATTATCTCGTTATGCAGATATTTCCGGGTG  
CATAGCATTGACAAATGCTCATAACAAAAGAAAATGTTTTATATGAAGAGTTTTGTAAACT  
GTCGTGTCTGTTTAGCGGAAAGTTTTAAAAAGTATGSAATTAACAAAACGACACAAATAGC  
GGTGTGTAGCGAAAATGGTCTGCAATTTTTCTTCTGTAAATGCATCATTGTATCTTGG  
AATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGG  
TATTGTAAAACACGCATAGTTTTTTGTCCAAGAATACTTTTCAAAAAGTACTGAATGT  
40 AAAATCTAAATTAATAATCTATTGAACTATTATTATATTAGACTTAAATGAAGACTTAGG  
AGGTTATCAATGGCTCAACAACCTTTATTTCTCAAAATTCGATAGTAATTCGGACGTAA  
AAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTATGTTTTCTTC  
TGTACAACTGGTCTGCGGAAGGGAGTCATGCTAACTCACAAGAAATATTGTGCAGGATT  
TTCTCTTGCAAAAGATCTTACTTTTGGTAACGCAATTAATCCACGACAGCAATTTTAACT  
45 GGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGG  
ATTCCGAGTGTCTTAATGCACACGTTTGAAGAAAAACTATTCTACAAATCATTACAAGA  
TTATAAGTGGAAAGTACTTTACTTGTACCAACATTAATGGCATTCTTGGCAAAAAGTGT  
ATTAGTTGAAAAGTACGATTTATCCCACTTAAAGAAATTCATCTGGTGGGCACTTTT  
ATCAAAAGAAATTTGGGGAGATGGTGAAAAAACGTTTTAAATTAACCTTTGTGAGCAAGG  
50 STATGGATTAACAGAAACCACTTGGCTGTTTTTAATTACACCGAAAGGTGAGGCCAAAC  
GGGATCAACTGTTAAATAAGTACCTTTTCAAGCTGTAAAGTTGTGATCTTACAACAGG  
AAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTTAAAGGCGCGATGATAATGAA  
1200

	GGTTATTATAATAATGAAGAACTACTAAAGCAATTATTGATAATGACGGATGGTTGGG	1280
	CTGTGGTGATATTGCTTATTATGACAAATGATGGCCATTTTATATTGTGGACAGGCTGAA	1320
	GTCTACTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAGGGAATACTCTT	1360
	ACAACATCCGTATATTGTTGATGCCGGGCTTACTGGTATACCGGATGAAGCCGCGGGGA	1400
5	GCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAAAAATATCTAAACGAACAAATCGTACA	1440
	AGATTATGTTGCCAGTCAAGTTTCAACAGCCAAATGGCTACCTGGTGGGTCGAAATTTTT	1480
	GGATGAAATTCCCAAAGGATCAACTGGAAAAATTGACAGAAAAGTGTTAAGACAAATGTT	1520
	TGAAAAACACACCAATGGG	1560

10 133-1B2 (SEQ ID NO:7)

	AGATCCAATGGCAGATAAGAATATTTTATATGGGCCCGAACCATTTTATCCCTTGGAAAG
	ATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATATTCCGGGC
	TGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTTATATGAAGAGTTTCTGAA
	ACTGTCTGTCTGTTTAGCGGAAAGTTTTAAAAAGTATGGATTAAAAACAAAACGACACAA
15	TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCTCTGTAATTGCATCATTGTAT
	CTTGGAAATAATTGTGGCACCTGTTAACGATAAAATACATTGAACGTGAATTAATACACAG
	TCTTGSTATTGTAAAACACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTAC
	TGAATGTAAAATCTAAATTAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAT
20	GACTTAGGAGGTTATCAATGCTCAACAACCTTTATTTCTCAAAAATTCCGATAGTAATCT
	GGACGTAAAAAAATTTAAACCATATTCCTTTAATCGAGACGATCAGGTTGCGTTGATTA
	TGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACTCACAAGAATATT
	GTTGCACGATTTTCTATTGCAAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGTC
	AGCAATTTTAAACGGTAATACCTTTCCACCATGGTTTTGGTATGATGACCACATTAGGAT
	ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAACTATTTCTA
25	CAATCATTACAAGATTATAAAGTGGAAAGTACTTTACTTGTACCAACATTAAATGSCATT
	TCTTGCAAAAAGTGCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGSCAT
	CTGGTGGCGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
	AACTTTGTCAAGGCAAGGGTATGGATTAAACAGAAACCACTTCGGCTGTTTTAATTACACC
	GAAAGGTGACGCCAAACCGGGATCAACTGGTAAAATAGTACCATTTACCGCTGTTAAAG
30	TTGTGATCCTACAAACAGGAAAAATTTGGGGCCAAATGAACCTGGAGAATTGATTTTT
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35	TATACCGGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAA
	AATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTCAAAAGTAAA
	TGGCTACGTGGTGGGGTGATATTTTTGGATGAAATTCCCAAAGGATCAACTGGAAAAAT
	TGACAGAAAAGTGTTAAGACAAATGTTAGAAAAACACACCAATGGG

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	GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCGAACCATTTTATCCCTTGGAAAG
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45	TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCTCTGTAATTGCATCATTGTAT
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	TCTTGSTATTGTAAAACACGCATAGTTTTTTTGTCTCAAAAGTAATACTTTTCAAAAAGTAC
	TGAATGTAAAATCTAAATTAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAA
	GACTTAGGAGGTTATCAATGCTCAACAACCTTTATTTCTCAAAAATTCCGATAGTAATCT
50	GGACGTAAAAAAATTTAAACCTATTCTTTTAAATCGAGACGATCAGGTTGCGTCGATTA

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TGTTTTCTTCTGGTACAACCTGGTCTGCCGAAGGGAGTCATGCTAACTCACAAGAATATT  
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